

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SUN, Yi
- (ii) TITLE OF INVENTION: SAG: Sensitive to Apoptosis Gene
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Warner-Lambert Company
 - (B) STREET: 2800 Plymouth Road
 - (C) CITY: Ann Arbor
 - (D) STATE: Michigan
 - (E) COUNTRY: USA
 - (F) ZIP: 48105

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/509,779
- (B) FILING DATE: 03-29-2000

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: David R. Kurlandsky
- (B) REGISTRATION NUMBER: 41,505
- (C) REFERENCE/DOCKET NUMBER: 5650-01-DRK

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 734-622-7304
- (B) TELEFAX: 734-622-1553

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..355

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: $17..\overline{3}55$

6

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC G Met Ala Asp Val Glu Asp G 1 5		49
GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser 15 20		97
AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val		145
GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg 45	GGTC CAG GTG ATG GAT Val Gln Val Met Asp 55	193
GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln 65 70	Glu Asp Cys Val Val	241
GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC Val Trp Gly Glu Cys Asn His Ser Phe His Asn 80		289
TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys 95 100		337
GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCG Val Gln Arg Ile Gly Lys 110	CT CCTGGTGTGG	385
TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC	ATCCTTGAGA GAGAGAGGAT	445
GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA	ATTTGTCTGT TTAGTTTTGG	505
GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT	TTCCTACCTC TGGTGTGTGT	565
GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA	TGATCTTTGT TTATCTGTAC	625
CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG	TGTTTATGCT TGAGGGTTAA	685
AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA	TTGAAAAGCC GACTCCTCCT	745
AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC	TGCTGTCTTC ATTTGCTGTG	805
AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT	GTCGGGTAAA CTGTAATATG	865
GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC	CATCTTTGAC TTGGCCAGGA	925

AGCCTGGATT	GTTCAACCAC	TTAGTTCTAA	AGAACTGTTT	TCTGTTTTTG	CCGAAGGTTG	985
TATTGTATGT	TTTAGTCAAA	AATATTAGTA	GGAAAATGGC	TTACTAGTAT	AACACTGAAG	1045
TTCATTATGC	AATGTTTTAA	TAAAATATTG	TGCTTTGAGT	TATTAAAGTT	TGATATATAC	1105
TCTTAAAATC	ATTAAACTAA	TTCATCAATT	AAATG			1140

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His 1 5 10 15

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339

	(B) LOCATION:1339	
BI.	<pre>(ix) FEATURE:</pre>	17
V	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	•
	ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
	TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
	AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	144
`	ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60	192
	CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT GIn Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 70 75	240 237
	AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
	AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
	AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	389
	TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
	GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
	ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
	TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629

749

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

TTAAA 754

- (2) INFORMATION FOR SEQ ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTR

18

(2) INFORMATION FOR SEQ ID NO: 6:

	(A) LENGTH: 13 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "Oligonucleotide: P2	
upstre	eam primer"	
(xi) L _{AAGCTTNI}	SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
		13
	DRMATION FOR SEQ ID NO: 7:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
CGGGATC	CCC ATGGCCGACG TGAGG	25
(2) INFO	DRMATION FOR SEQ ID NO: 8:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
CGGGATC	CTC ATTTGCCGAT TCTTTG	26
(2) INFO	DRMATION FOR SEQ ID NO: 9:	
(i)	SEQUENCE CHARACTERISTICS:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide P.01" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: TATGGCTAGC ATGGCCGACG TGGAGG (2) INFORMATION FOR SEQ ID NO: 10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...270
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC

48

26

Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His	
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	AAG Lys	ATG Met	TTC Phe 30	TCC Ser	CTC Leu	96
								TGG Trp								144
								ATG Met								192
								TGG Trp								240
								TGT Cys		TGA	AACAG	GAA (CAAT	CGCT	GC .	· 290
CCT	CTCTC	GCC A	AGCA	GACT	rg go	TGGT	CCA	A AGA	ATC	GCA	AATO	SAGAC	STG (STTAC	SAAGGC	350
TTCT	TAGO	CGC A	AGTTO	STTCA	AG AG	SCCCI	GGT	GAT	СТТС	TAA	TCC	AGTGC	ccc :	[ACA	AGGCT	410
AGAZ	ACACI	TAC A	AGGGG	SATGA	AA TI	CTTC	CAAA	r Ago	AGCC	CGAT	GGA'	CTGI	GG :	CTTT	GGACT	470
CATO	CAAAC	GCC 1	TGG1	TAGO	CA TI	TGT	AGTI	TTA	ATCTT	CAG	AAA	TCTC	CTG :	rgat1	'AAGAA	530
GATA	ATTI	TAT	CAAA!	GTG	T C	CTTCC	CTACC	TC1	GTG	STGT	GTGT	rcgco	CA (CACAC	CTTAG	590
AAGI	GCTA	ATA A	\AAA.	AGGAZ	AA GA	AGCTO	CAAA	A TTC	SAATO	CACC	TTAT	TAAT1	TA (CCCAT	TTCTA	650
TACA	ACAG	GGC A	AGTGG	SAAGO	CA GI	TTC	AGAC	TTI	TTC	ATG	CTTA	ATGGI	TG A	ATCAC	TTAAA	710
AAA	AATO	STT A	ACAGI	'AAC	LA A	'AAA	TGC	A GTT	TAAZ	A.						747

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu 50 55 60

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile 65 70 75 80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly 85 90

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..291

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: $1...2\overline{9}1$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

					GAC Asp											48
					TCC Ser											96
					GTG Val											144
					AGG Arg											192
					AAC Asn 70											240
AAT Asn	CGC Arg	TGC Cys	CCT Pro	CTC Leu 85	TGC Cys	CAG Gln	CAG Gln	GAC Asp	TGG Trp 90	GTG Val	GTC Val	CAA Gln	AGA Arg	ATC Ile 95	GGC Gly	288

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	341
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	401
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	461
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	521
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	581
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	641
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	701
TTAAA	706
(2) INFORMATION FOR SEQ ID NO: 14:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 97 amino acids(B) TYPE: amino acid	

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys 50 55 60

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 65 70 75 80

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 85 90 95

Lys

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

	(11)	(A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
GCC	CATCTG	CA GGGTCCAG	18
(2)	INFO	RMATION FOR SEQ ID NO: 16:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
J/	(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
GGA	TCCTC	AT TTGCCGATTC TTTGGAC	27
(2)	INFO	RMATION FOR SEQ ID NO: 17:	
	(i) -	SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
S		MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide XX4-5"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
TTC	TCCAG	G GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC	58
(2)	INFO	RMATION FOR SEQ ID NO: 18:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(D) TOPOLOGY: linear

	4 –	∙3"	(A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
	ACCT	'CGGT	AT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG	59
	(2)	INFO	RMATION FOR SEQ ID NO: 19:	
	f	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
~		(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
	TTCT	'CCAG'	TG GCAGAGAAC	19
	(2)	INFO	RMATION FOR SEQ ID NO: 20:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
	ATGA	ATTT	AA TGTTTACGGG C	21
	(2)	INFO	RMATION FOR SEQ ID NO: 21:	
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: cDNA	

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE: (A) NAME/KEY: mat peptide (B) LOCATION: 1...339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21: ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 10 TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 25 AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 ACG AGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192 Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 55 CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 70 AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA 389 Lys TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629 GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689 TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749 TTAAA 754

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

- (2) INFORMATION FOR SEQ ID NO: 22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

- (2) INFORMATION FOR SEQ ID NO: 23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...339
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1...339
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

						GGA Gly										48
						AAG Lys										96
			Asn			GCC Ala										144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	AGC Ser	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys	192
						GAG Glu										240
						TGC Cys										288
						CAG Gln										336
AAA Lys	TGAG	AGTO	GT I	TAGAZ	\GGC1	T CI	TAGO	CGCAG	TTC	STTC <i>I</i>	AGAG	CCCI	rggro	GA.		389
TCTT	GTA	ATC C	CAGTO	CCCI	'A CA	AAGG	CTA	AAC	CACTA	ACAG	GGG	ATGAZ	ATT C	CTTC	\AATAG	449
GAG	CCGAT	GG A	ATCT	TGGT	C TI	TGGA	ACTC	A TCF	AAGC	CTT	GGTT	AGC	ATT I	GTC	AGTTTT	509
ATCI	TCAG	SAA A	ATTCI	CTGT	'G A'I	TAAC	SAAGA	A TAP	TTTÆ	ATTA	AAGO	TGGT	CC I	TCCI	ACCTC	569
TGT	GTGI	GT G	TCGC	CGCAC	CA CA	AGCTI	AGAA	A GTG	CTAT	'AAA'	AAA	GAAA	AGA G	CTCC	CAAATT	629
GAAT	CACC	CTT A	TAAT	TTAC	CC CA	TTTC	TATA	A CAP	CAGG	CAG	TGGA	AGC	AGT I	TCGA	AGACTT	689
TTTC	GATO	CT I	ATG	TTGA	AT CA	\GTTA	AAAA.	A AGA	ATGI	TAC	AGTA	ACAZ	AAT A	AAGI	GCAGT	749
TTAA	AA .															754

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His	
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu	
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Cys	Asp	
Thr	Cys 50	Ala	Ile	Ser	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Суѕ	Leu	Arg	Cys	
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	His 85	Asn	Суѕ	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INFO	RMAT	rion	FOR	SEQ	ID 1	NO: 2	25:								
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA															
	(11) NOBBOOKE IIIB. CDMA															
	(ix)	(P	ATURI A) NA B) LO	ME/F			39									
	(ix)	(P	ATURE A) NA B) LO	ME/I		.	_pept 39	cide								
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ I	ID NO	D: 25	ō:			•		
ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His	48
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	AAG Lys	ATG Met	TTC Phe 30	TCC Ser	CTC Leu	96
AAG Lys	AAG Lys	TGG Trp	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val	GAG Glu	TGC Cys	GAT Asp	144

			ATC Ile													192
			AAC Asn													240
			TTC Phe													288
			CCT Pro 100													336
AAA Lys	TGAG	SAGTO	GT I	TAGAZ	AGGCI	T CI	TAGO	CGCA	TTC	STTCA	AGAG	CCCI	GGT	GGA		389
TCTI	GTAA	ATC (CAGTO	CCCI	'A CA	AAGG	CTAG	AAC	CACTA	ACAG	GGGA	TGA	ATT (CTTCA	AATAG	449
GAGO	CGAT	GG A	ATCTO	TGGT	C TI	TGGA	CTCF	A TC	AAGC	CTT	GGTI	'AGCA	TT T	rgtc <i>i</i>	GTTTT	509
ATCI	TCAG	SAA A	ATTCI	C T Gİ	G AI	TAAC	SAAGA	A TAA	ATTT <i>F</i>	ATTA	AAGG	TGGT	CC 1	TCCI	ACCTC	569
TGTG	GTGI	GT (STCGO	CGCAC	CA CA	AGCTI	'AGAA	A GT	CTAI	'AAA	AAA	GAAA	AGA (GCTCC	TTAAA	629
GAAT	CACC	CTT A	raat <i>i</i>	TTAC	CC CA	TTTC	TATA	CAA	ACAGO	GCAG	TGGA	AGCA	AGT T	TCG	GACTT	689
TTTC	GAT	CT 1	TATGO	GTTG#	AT CA	\GTT#	AAAA	A AGA	ATGI	TAC	AGTA	ACAZ	AT A	\AAG1	GCAGT	749
TTAA	ιA															754

40

(2) INFORMATION FOR SEQ ID NO: 26:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

	50					55					60					
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	His 85	Asn	Cys	Суз	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INFO	ORMA!	CION	FOR	SEQ	ID 1	10: 2	27:								
	(i)	() () ()	3) TY C) ST O) TO	ENGTI YPE: FRANI OPOLO	H: 75 nucl DEDNE	54 ba Leic ESS: line	ase p acid doub ar	pairs d	5							
	(ii)	MO]	LECUI	LE TY	YPE:	cDNA	A									
	(ix)	(]	ATURI A) NA 3) LO	AME/I			39									
	(ix)	(2	ATURI A) NA 3) LO	AME/I		_		tide								
	(xi)	SEÇ	QUENC	CE DI	ESCRI	[PTIC	ON:	SEQ :	ID NO	D: 2	7:					
								GAA Glu								48
								GGA Gly 25								96
								TGG Trp								144
								GTG Val								192
								TGT Cys								240

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC

ASII	1113	Ser	the	85	VSII	Суѕ	Cys	Mec	90	ьеи	пр	vai	гуѕ	95	ASII
AAT Asn	CGC Arg	TGC Cys	CCT Pro 100	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp 105	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg 110	ATC Ile	GGC Gly
AAA Lys	TGA	GAGT(GGT (raga <i>i</i>	AGGC'	TT C	TTAG(CGCA	G TT(GTTC <i>l</i>	AGAG	CCC	rggt(GGA	
TCTT	rgta/	ATC (CAGTO	GCCCI	ra ca	AAA G(GCTA	S AAG	CACTA	ACAG	GGG	ATGA	ATT (CTTC	AAATAG
GAG	CCGA	rgg A	ATCTO	GTGGT	rc T	rtgg/	ACTC	A TC	AAAG	CCTT	GGT	FAGC	ATT :	FGTC	AGTTTT
ATC	TCA	GAA A	ATTC:	rctgi	rg A	CAATI	GAAG?	A TA	ATTT?	ATTA	AAG	GTGG:	rcc :	TTCC:	TACCTC
TGT	GTG	rgr (T CG	CGCA	CA CA	AGCT	raga <i>i</i>	A GT	GCTA:	raaa	AAA	GGAA.	AGA (GCTC	CAAATT
GAA'	CAC	CTT A	ATAA	TTAC	CC CZ	ATTT	CTATA	A CAA	ACAGO	GCAG	TGG	AAGC	AGT '	rtcg/	AGACTT
TTTC	CGAT	GCT T	TATG	GTTG#	AT C	AGTTA	AAAA	A AGA	AATG	TAC	AGT	AACA?	AAT Z	AAAG'	rgcagt
TTA	λA														
(2)	INFO	ORMA:	TION	FOR	SEQ	ID i	NO: 2	28:							
		(<i>1</i>	A) LI 3) T		4: 11 amir	13 ar									
		MOI SEQ					tein ON: S	SEQ]	D NO	D: 28	3:				
Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Суѕ	Asp
Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Ser	Leu	Arg	Cys
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Суѕ	Val	Val 75	Val	Trp	Gly	Glu	Cys 80
Asn	His	Ser	Phe	His 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

	(1)	() ()	A) L1 B) T' C) S'	ENGTI YPE: FRANI	nuci DEDNI	CTERI 54 ba leic ESS: line	ase p acid doub	pair: d	5							~
	(ii)) MO	LECU:	LE T	YPE:	cDNA	A									2
	(ix)		A) N2	AME/		CDS	39									
	<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:</pre>															
	(xi)) SE(QUEN	CE DI	ESCR:	IPTIC	ои: :	SEQ :	ID NO	D: 29	9:					
ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His	48
						AAG Lys										96
						GCC Ala										144
						GTC Val 55										192
						GAG Glu										240
			Phe	His	Asn	TGC Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	288
AAT Asn	CGC Arg	TGC Cys	CCT Pro 100	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp 105	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg 110	ATC Ile	GGC Gly	336
AAA Lys	TGA	GAGT(GGT :	raga <i>i</i>	AGGCT	rt Ci	TTAG(CGCA	G TT	GTTC?	AGAG	ccc	rggt	GGA.		389

TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG	449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA	•					754

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1...339 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1...339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31: ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 10 TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 70 AAT AAA TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288 Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 90 AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA 389 Lys TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

689

749

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

- (2) INFORMATION FOR SEQ ID NO: 32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

- (2) INFORMATION FOR SEQ ID NO: 33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339
 - (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met	GCC Ala	GAC Asp	GTG Val	Glu	GAC Asp	GGA Gly	GAG Glu	GAA Glu	Thr	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser	CAC His	48
1	GGG	ACC	ጥሮል	5 ecc	ጥሮሮ	አአር	ጥሮር	CCA	10	CAC	7 7 C	» m.c	mmc	15 TCC	стс	0.0
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu	96
														TGC Cys		144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys	192
CAA Gln 65	GCT Ala	GAA Glu	AAC Asn	AAA Lys	CAA Gln 70	GAG Glu	GAC Asp	TGT Cys	GTT Val	GTG Val 75	GTC Val	TGG Trp	GGA Gly	GAA Glu	TGT Cys 80	240
AAT Asn	CAT His	TCC Ser	TTC Phe	AAG Lys 85	AAC Asn	TGC Cys	TGC Cys	ATG Met	TCC Ser 90	CTG Leu	TGG Trp	GTG Val	AAA Lys	CAG Gln 95	AAC Asn	288
AAT Asn	CGC Arg	TGC Cys	CCT Pro 100	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp 105	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg 110	ATC Ile	GGC Gly	336
AAA Lys	TGAG	SAGTO	GT I	'AGA	AGGCI	T CI	TAGO	CGCAG	TTC	STTCA	AGAG	CCCT	rggT	GGA		389
rcti	'GTAA	ATC C	CAGTO	CCCI	'A CA	AAAGG	CTA	AAC	CACTA	ACAG	GGG	TGA	ATT ·	CTTCA	\AATAG	449
GAGC	CGAT	GG A	ATCT	FTGGT	с тл	TGG	ACTC	A TCF	AAAGO	CTT	GGTI	'AGC	ATT '	TGTC	\GTTTT	509
															TACCTC	
															CAAATT	
															AGACTT	
		CT I	ATGG	TTGA	AT CA	AGTTA	LAAA	A AGA	ATGI	TAC	AGTA	ACAZ	AT I	AAAGI	GCAGT	749
TTAA	A															754

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 10 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 40 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 90 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 Lys (2) INFORMATION FOR SEQ ID NO: 35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1...339 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1...339
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

20 25 30

			AAC Asn													144
			ATC Ile													192
			AAC Asn													240
			TTC Phe													288
			CCT Pro 100													336
AAA Lys	TGAG	GAGT(GGT 1	raga <i>i</i>	AGGCT	гт ст	TTAGO	CGCA	TTC	STTC <i>i</i>	AGAG	CCCI	rggt	GGA		389
TCTI	GTA	ATC (CAGTO	GCCC	TA CA	\AAG(CTA	AAC	CACTA	ACAG	GGG	\TGA#	ATT (CTTCA	AAATAG	449
GAGO	CGAT	rgg i	ATCT	GTGGT	C T	TGG	ACTC	A TC	AAAGO	CCTT	GGTT	AGC	ATT :	TGTC#	AGTTTT	509
ATCI	TCAC	SAA J	ATTCT	CTG	G A	TAAC	SAAGA	A TAA	ATTT <i>I</i>	ATTA	AAGG	TGGT	rcc :	TTCCI	TACCTC	569
TGT	GTGT	GT (GTCG	CGCAC	CA CA	AGCTI	raga <i>i</i>	A GTO	CTAI	AAA	AAAG	GAAA	AGA (GCTC	CAAATT	629
GAAT	'CAC	CTT I	ATAAT	ATT	CC CA	ATTTC	CTATA	A CAA	ACAGO	CAG	TGGA	AAGCA	AGT :	TTCG#	AGACTT	689
TTTC	GAT	CT	TATGO	GTTG#	AT CA	AGTTA	XAAA/	A AGA	AATGI	TAC	AGTA	ACAZ	AAT A	AAAGI	GCAGT	749
TTAP	LΆ															754

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Cys	Leu	Arg	Cys	
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	His 85	Asn	Cys	Ser	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Суѕ	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys											•		-			
(2)	INFO	RMA'	rion	FOR	SEQ	ID N	10: 3	37:								
	(i)	(<i>I</i> (I	QUENCA) LE B) TY C) ST D) TO	ENGTH (PE: [RANI	H: 75 nucl	64 ba Leic ESS:	ase p acio douk	pair:	5							
	(ii)	MOI	LECUI	E TY	PE:	cDNA	Ą									
	(ix)	(1	ATURE A) NA B) LO	ME/F			39									
	(ix)	(Z	ATURE A) NA B) LC	ME/F				ide								
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: S	SEQ I	ID NO	o: 37	7:					
ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His	48
			TCA Ser 20													96
			AAC Asn													144
		35					40					45			_	
Thr	Cys 50	Ala	ATC Ile	Cys	Arg	Val 55	Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys	192
CAA Gln 65	GCT Ala	GAA Glu	AAC Asn	AAA Lys	CAA Gln 70	GAG Glu	GAC Asp	TGT Cys	GTT Val	GTG Val 75	GTC Val	TGG Trp	GGA Gly c	GAA Glu	TGT Cys 80	240

	r Phe His A		ATG TCC CTG Met Ser Leu		Gln Asn	288
7.7M CCC 7.CC	85		90		95	
			GAC TGG GTG Asp Trp Val 105		Ile Gly	336
AAA TGAGAG Lys	rggt tagaag	GCTT CTTAGO	CGCAG TTGTTC	AGAG CCCTGGT	'GGA	389
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	G AACACTACAG	GGGATGAATT	CTTCAAATAG	449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	A TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAZ	A GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	A CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA						754

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2)	INFORMATION	FOR	SEO	ID	NO:	39:

1	i) SEQUENCE	CHARACTERISTICS:
١			CITATACI ENTO LICO:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

Com

Lys

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: $1..3\overline{39}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

						GGA Gly									48
						AAG Lys									96
						GCC Ala									144
						GTC Val 55									192
						GAG Glu									240
						TGC Cys									288
						CAG Gln									336
AAA	TGAG	SAGTO	GT 1	AGAZ	AGGCI	т ст	TAGO	CGCA	TTC	STTCA	AGAG	CCCT	GGT	GA	389

TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG	449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGAC'IT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA						754

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(ii) MOLECULE TYPE: cDNA											
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339											
<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339</pre>											
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:											
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 .	48										
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96										
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144										
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA AGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser 50 55 60	192										
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240										
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288										
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336										
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	389										
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449										
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509										
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569										
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629										
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689										

(D) TOPOLOGY: linear

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

749

TTAAA

754

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His		48
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	AAG Lys	ATG Met	TTC Phe 30	TCC Ser	CTC Leu		96
AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	TGC Cys	GAT Asp		144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys		192
							GAC Asp										240
							TGC Cys										288
							CAG Gln										336
AAA Lys	TGAG	AGTG	GT T	'AGA	AGGCI	T CI	TAGO	GCAG	TT (STTCA	AGAG	CCCI	GGT	GA.			389
TCTI	GTAA	ATC C	CAGTO	CCCI	'A CA	AAAGG	CTAG	; AAC	ACTA	CAG	GGG	TGA	TT C	TTC	\AATAG	ł	449
GAGC	CGAT	GG A	ATCT	TGGT	C TI	TGGA	ACTCA	TCA	AAGC	СТТ	GGTI	AGCA	TT T	GTCA	AGTTTT	ı	509
ATCI	TCAG	SAA A	TTCI	CTGT	G AI	TAAC	SAAGA	TAP	TTTP	ATTA	AAG	TGGT	CC I	TCCI	ACCTC		569
TGT	GTGT	GT G	TCGC	GCAC	CA CA	AGCTI	'AGAA	GTG	CTAT	'AAA	AAA	GAAA	.GA ∙ G	CTCC	TTAAAC		629
GAAT	CACC	TT A	LAAT	TTAC	CC CA	TTTC	TATA	CAA	CAGG	CAG	TGGA	AGCA	GT I	TCGA	GACTT		689
TTTC	GATO	CT I	ATGO	STTGA	AT CA	AGTT <i>P</i>	AAAA	AGA	ATGI	TAC	AGTA	ACAP	AT A	AAGI	GCAGT		749
TTAA	A																754

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION:1..339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1 1 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

			AAC Asn													144
			ATC Ile													192
			AAC Asn													240
			TTC Phe													288
			CCT Pro 100													336
AAA Lys	TGA	GAGT(GGT 1	raga <i>i</i>	AGGCT	rt ci	TTAGO	CGCA	F TTC	STTC <i>I</i>	AGAG	CCCI	rggT(GGA		389
TCTT	rgta <i>i</i>	ATC (CAGTO	GCCT	ra ca	AA AG(GCTAC	AA E	CACTA	ACAG	GGGZ	ATGAZ	ATT (CTTCA	AAAT AG	449
GAGO	CCGAT	rgg Z	ATCTO	GTGGT	C T	rtgg/	ACTCA	A TCA	AAAG	CTT	GGTT	ragc <i>i</i>	ATT :	rgtc <i>i</i>	AGTTTT	509
ATCI	TCAC	GAA A	ATTCI	CTGT	rg An	TAAC	GAAGA	A TAZ	ATTT <i>I</i>	ATTA	AAGO	STGGT	rcc :	rtcci	TACCTC	569
TGT	GTGT	rgr (GTCG	CGCA	CA CA	AGCTI	ragaz	A GTO	CTAT	AAA	AAA	GAA/	AGA (GCTC	CAAATT	629
GAAT	CAC	CTT A	CAATA	ATTT	CC CA	ATTTC	CTATA	A CAA	ACAGO	CAG	TGG	AAGCA	AGT :	rtcg/	AGACTT	689
TTTC	CGATO	GCT :	ratg(STTGA	AT CA	AGTTA	AAA/	A AGA	ATGI	TAC	AGTA	A CAZ	AAT A	AAAG1	TGCAGT	749
TTA	AA.															754

30

(2) INFORMATION FOR SEQ ID NO: 46:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Cys	Asp	
Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Ser	Leu	Arg	Ser	
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	His 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INFO	RMAT	MOI	FOR	SEQ	ID 1	10: 4	17:								
	(i)	(<i>I</i> (<i>I</i>	A) LH B) TY C) ST	ENGTI PE:	H: 75 nucl	54 ba Leic ESS:	ISTIC ase p acic douk ear	oairs 1	3							
	(ii)	MOI	LECUI	E TY	PE:	cDNA	A									
	(ix)	(Z		E: AME/F DCATI			39									
	(ix)	(Z					_pept 39	ide								
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ 1	ED NO	D: 47	7:					
							GAG Glu									48
							TCG Ser									96
							ATG Met 40									144
							CAG Gln									192
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240

Gln 65	Ala	Glu	Asn	Lys	Gln .70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80
														CAG Gln 95	
														ATC Ile	
AAA Lys	TGA	GAGT(GGT :	[AGA]	AGGC	TT CT	rtag(CGCA	G TTC	GTTC/	AGAG	CCC	rggt	GGA	
TCT	rgta <i>i</i>	ATC (CAGT	GCCC.	ra ca	AAAG	GCTA(G AAG	CACTA	ACAG	GGGZ	ATGA/	ATT (CTTCA	AAATAG
GAG	CCGA!	rgg A	ATCT	GTGG:	C T	rtgg/	ACTCA	A TC	AAAG	CCTT	GGT	ragc <i>i</i>	ATT :	rgtca	AGTTTT
ATC	TTCA	GAA A	ATTC:	rctg:	rg An	PAATI	GAAGA	A TAZ	ATTT?	ATTA	AAG	STGGT	rcc :	rtcci	TACCTC
TGT	GGTG:	rgr (GTCG	CGCA	CA CA	AGCTT	raga <i>i</i>	A GTO	CTAT	raaa	AAA	GAA.	AGA (GCTC	CAAATT
GAA:	rcac(CTT A	ATAA	TTA	CC CA	ATTTC	CTATA	A CAA	ACAGO	GCAG	TGG	AAGC	AGT :	rtcg <i>i</i>	AGACTT
TTT	CGAT	GCT T	ratgo	GTTG/	AT CA	AGTT?	XAAA/	A AGA	ATG	TAC	AGT	AACAZ	ÄT A	AAAGI	rgcagt
TTA	AA.														
(2)	INF	ORMA:	rion	FOR	SEQ	ID N	10: 4	18:							
		(<i>I</i>	A) Li B) T	ENGTI YPE:	H: 13	RACTE 13 am no ac line	nino cid								
						prot [PTIC		SEQ 1	D NO): 48	3:				
Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Cys	Asp
Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Cys	Leu	Arg	Cys
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80
Asn	His	Ser	Phe	His 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn

Asn	Arg	Ser	Pro 100	Leu	Ser	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	, : OK	49:								
	(i)	(1	A) L1 B) T1 C) S1	CE CI ENGTI YPE: FRANI OPOLO	i: 75 nucl DEDNI	54 ba Leic ESS:	ase p acio doub	pair:	5							
1	(ii)) MOI	LECU	LE T	PE:	CDNZ	A									
	(ix)	(2		E: AME/I OCATI			39									
	(ix)	(2		E: AME/I OCATI				cide								
	(xi)	SEÇ	QUEN	CE DI	ESCRI	· [PTI	ON: S	SEQ I	ID NO	D: 49	9:					
				GAA Glu 5												48
				GGC Gly												96
AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	AGC Ser	GAT Asp	144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys	192
CAA Gln 65	GCT Ala	GAA Glu	AAC Asn	AAA Lys	CAA Gln 70	GAG Glu	GAC Asp	TGT Cys	GTT Val	GTG Val 75	GTC Val	TGG Trp	GGA Gly	GAA Glu	TGT Cys 80	240
				CAC His 85												288
AAT Asn	CGC Arg	TGC Cys	CCT Pro	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg	ATC Ile	GGC Gly	336

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGA Lys	G CCCTGGTGGA 389									
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GG	GATGAATT CTTCAAATAG 449									
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GG	TTAGCATT TGTCAGTTTT 509									
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AA	GGTGGTCC TTCCTACCTC 569									
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AA	AGGAAAGA GCTCCAAATT 629									
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TG	GAAGCAGT TTCGAGACTT 689									
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AG	TAACAAAT AAAGTGCAGT 749									
TTAAA	754									
(2) INFORMATION FOR SEQ ID NO: 50:										
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 113 amino acids										
(B) TYPE: amino acid										
(D) TOPOLOGY: linear										
(ii) MOLECULE TYPE: protein										
/ CECHENCE DECOREDETON, COO. TO NO. CO										

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys